## CLAIMS

What is claimed is:

1        1.      A method for estimating the precision of measurements taken from an

2 array, comprising:

3        (a)      identifying a set of low-level data measurements;

4        (b)      estimating a standard deviation, $\sigma_\varepsilon$ of an additive error component, $\varepsilon$;

5        (c)      estimating a background parameter, $\alpha$;

6        (d)      identifying a set of replicated high-level data measurements;

7        (e)      estimating a standard deviation, $\sigma_\eta$ , from the standard deviation of

8                  the logarithm of the replicated high-level data set;

9        (f)      measuring a signal, $y$, wherein said signal indicates an amount of a

10                  biological molecule; and

11       (g)      estimating a variance of the measured signal as

12      $\text{Vâr}(\hat{\mu}) = \hat{\sigma}_\varepsilon^2 + \hat{\mu}^2 e^{\hat{\sigma}_\eta^2}\left(e^{\hat{\sigma}_\eta^2} - 1\right)$, where $\hat{\mu}^2 = (y - \alpha)^2$.

1        2.      The method of claim 1, wherein said identifying step (a) comprises the

2 use of a thresholding algorithm to establish a cutoff, and the set of low-level data

3 consists of those data with values less than the cutoff.

1        3.      The method of claim 2, wherein the thresholding algorithm comprises

2 the steps of:

3        (a)      identifying $A_N$, an initial set of low-level data measurements consisting

4                  of $q$ percent of the total number of data points having the lowest

5                  measurement values, $A_N = \{x_1, x_2, \ldots, x_{no}\}$;

6        (b)      calculating a mean and a standard deviation of the initial set;

7        (c)      calculating a cutoff point, $u_N$ = mean plus $c$ x the standard deviation,

8                  wherein $2 \leq c \leq 3$;

9        (d)      defining a new set, $A_{N+1} = \{x_j < u_N\}$;

10       (e)      calculating a mean and standard deviation of the new set; and

11       (f)      repeating steps (c) and (d) using the mean and standard deviation of the

12                  new set until the algorithm converges.

1        4.      The method of claim 2, wherein the thresholding algorithm comprises

2 the steps of:

3    (a)    identifying $A_N$, an initial set, of low-level data consisting of $q$ percent

4          of the total number of data points having the lowest measurement

5          values, $A_N = \{x_1, x_2, \ldots, x_{no}\}$;

6    (b)    calculating a median of the initial set, $m_0 = \text{median} \left\{x_j\right\}_{j=1}^{n_o}$ and a

7          median of the absolute deviations about the median,

8          $MAD_0 = \text{median} \left\{\left|x_j - m_o\right|\right\}_{j=1}^{n_o}$;

9    (c)    calculating a cutoff point, $u_0 = MAD_0 + c \times s_0$, wherein $s_0 =$

10         $MAD_0/0.675$ and $2 \leq c \leq 3$;

11   (d)    defining a new set, $A_{N+1} = \{x_j < u_N\}$;

12   (e)    calculating a median and a median of the absolute deviations about the

13         median of the new set; and

14   (f)    repeating steps (c) and (d) using the median and the median of the

15         absolute deviations about the median of the new set until the algorithm

16         converges.

1    5.    The method of claim 2, wherein the mean of the low-level data

2    measurements is used as the estimate of the background parameter, $\alpha$.

1    6.    The method of claim 1, wherein the standard deviation of the low-level

2    data measurementsis used as the estimate of the parameter $\sigma_\varepsilon$.

1    7.    The method of claim 1, wherein, a mean of negative control data is

2    used as the estimate of the background parameter, $\alpha$.

1    8.    The method of claim 1, wherein the biological molecule is a nucleic

2    acid.

1    9.    The method of claim 8, wherein the nucleic acid is mRNA.

1    10.   The method of claim 8, wherein the biological molecule is DNA.

1    11.   The method of claim 10, wherein the DNA is cDNA.

1    12.   The method of claim 10, wherein the DNA is genomic.

1    13.   The method of claim 1, wherein the biological molecule is a protein.

1    14.   The method of claim 1, wherein the biological molecule is a lipid.